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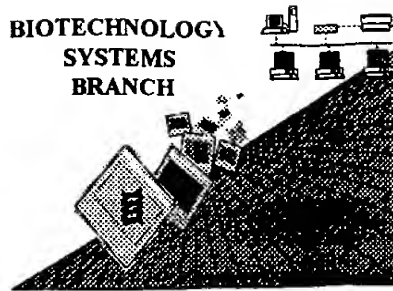
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11

BIOTECHNOLOGY
SYSTEMS
BRANCH**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/262,126A

Source: 1652

Date Processed by STIC: 2/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

FEB 14 2001

1652

TECH CENTER 1600/2500

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/262,126ADATE: 02/05/2001
TIME: 14:10:04Input Set : A:\GC396-2 seq.txt
Output Set : N:\CRF3\02022001\I262126A.rawDoes Not Comply
Corrected Diskette Needed

pp 1-2, 5

3 <110> APPLICANT: Miller, Brian S.
4 Shetty, Jayarama K.
6 <120> TITLE OF INVENTION: Modified Forms of Pullulanase
9 <130> FILE REFERENCE: GC396-2
11 <140> CURRENT APPLICATION NUMBER: 09/262,126A
12 <141> CURRENT FILING DATE: 1999-03-03
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2794
20 <212> TYPE: DNA
21 <213> ORGANISM: B. deramificans
23 <221> NAME/KEY: misc_feature
24 <222> LOCATION: (1)...(2794)
25 <223> OTHER INFORMATION: n = A, T, C, or G
27 <400> SEQUENCE: 1

28 gatgggaaca cgacaacgat cattgtccac tattttttgcc ctgctggtga ttatcaacct 60
29 tggagtctat ggatgtggcc aaaagacgga ggtggggctg aatacgattt caatcaacctg 120
30 gctgactctt ttggagctgt tgcaagtgtc gatattccag gaaacccaag tcaggtagga 180
31 attatcgttc gcaactcaaga ttggaccaa gatgtgagcg ctgaccgcta catagattta 240
32 agcaaaaggaa atgaggtgtg gcttgtagaa ggaaacagcc aaatttttta taatgaaaaa 300
33 gatgctgagg atgcagctaa acccgctgta agcaacgctt atttagatgc ttcaaaccag 360
34 gtgctgggta aacttagcca gccgttaact cttggggaag gnnnaagcgg ctttacgggt 420
35 catgacgaca cagcaaataa ggatattcca gtgacatctg tgaaggatgc aagtcttggg 480
36 caagatgtaa ccgctgtttt ggcaggtaac ttccaacata tttttggagg ttccgattgg 540
37 gcaectgata atcacagtac ttattataaa aaggtgacta acaatctcta tcaattctca 600
38 ggagatcttc ctgaaggaaa ctaccaatat aaagtggctt taaatgatag ctggaataat 660
39 ccgagttacc catctgacaa cattaattta acagtccctg ccggcggtgc acacgtcact 720
40 ttttcgtata ttccgtccac tcatgcagtc tatgacacaa ttaataatcc taatgcggat 780
41 ttacaagtag aaagcggggt taaaacggat ctctgtacgg ttactctagg ggaagatcca 840
42 gatgtgagcc atactctgtc cattcaaaaca gatggtctatc aggcaaagca ggtgatacct 900
43 cgtaatgtgc ttaattcatc acagtactac tattcaggag atgatcttgg gaatacctat 960
44 acacagaaag caacaacctt taaagtctgg gcaccaactt ctactcaagt aaatgttctt 1020
45 ctttatgaca gtgcaacggg ttctgtataa aaaatcgtac ctatgaacgg atcggggccat 1080
46 ggtgtgtggg aagcaacggg taatcaaaac cttgaaaatt ggtattacat gtatgaggta 1140
47 acaggccaag gctctaccog aacggctgtt gatccttatg caactgcgat tgcaccaaatt 1200
48 ggaacgagag gcatgattgt ggacctggct aaaacagatc ctgctggctg gaacagtgat 1260
49 aaacatatta cgccaaagaa tatagaagat gaggtcatct atgaaatgga tgtccgtgac 1320
50 ttttccattg accctaattc gggatatgaa aataaaggga agtatttggc tcttacagaa 1380
51 aaaggaaaca agggccctga caacgtataa acggggatag attccttaaa acaacttggg 1440
52 attactcatg ttacagctat gcctgttttc gcatctaaca gtgtcgatga aactgatcca 1500
53 acccaagata attgggggta tgacctcgc aactatgatg ttctgaagg gcagtatgct 1560
54 acaaatgcga atggtaatgc tcgtataaaa gagtttaagg aaatgggtct ttcactccat 1620
55 cgtgaacaca ttgggggttaa catggtatgt gtctataatc atacctttgc caccgaaatc 1680
56 tctgacttcg ataaaattgt accagaatat tattaccgta cgatgatcca ggtaattata 1740
57 ccaacggatc aggtactgga aatgaaattg cangcngaaa ggccaatggt tcaaaaattt 1800
58 attattgatt cccttaagta ttgggtcaat gagtatcata ttgaacggctt ccgttttgac 1860

→ <2207 ← insert this MANDATORY numeric identifier whenever <2217, <2227, or <2237 is shown

RAW SEQUENCE LISTING

DATE: 02/05/2001

PATENT APPLICATION: US/09/262,126A

TIME: 14:10:04

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02022001\I262126A.raw

59 ttaatggcgc tgcttggaaa agacacgatg tccaaagctg cctcggagct tcatgctatt 1920
 60 aatccaggaa ttgcacttta cgggtgagcca tggacgggtg gaacctctgc actgccagat 1980
 61 gatcagcttc tgacaaaagg agctcaaaaa ggcatgggag tagcgggtgtt taatgacaat 2040
 62 ttacgaaacg cgcttggacg caatgtcttt gattcttccg ctcaagggtt tgcgacaggt 2100
 63 gcaacaggct taactgatgc aattaagaat ggcgttgagg ggagtattaa tgactttacc 2160
 64 tcttoaccag gtgagacaat taactatgtc acaagtcacg ataactacac ccttggggac 2220
 65 aaaatagccc taagcaatcc taatgattcc gaagcggatc ggattaaaaat ggatgaactc 2280
 66 gcacaagcag ttgttatgac ctcacaaggc gttccattca tgcaaggcgg ggaagaaatg 2340
 67 cttcgtanaa aaggcggcaa cgacaatagt tataatgcag gcgatgcggg caatgagttt 2400
 68 gattggagca ggaaagctca atatccagat gttttcaact attatagcgg gctaatccac 2460
 69 cttcgtcttg atcaccacgc cttccgcacg acgacagcta atgaaatcaa tagccacctc 2520
 70 caattcctaa atagtccaga gaacacagtg gcctatgaat taactgatca tgtaataaaa 2580
 71 gacaaatggg gaaatatcat tgttgittat aaccocaaata aaactgtagc aaccatcaat 2640
 72 ttgccgagcg ggaaatgggc aatcaatgct acgagcggta aggtaggaga atccaccctt 2700
 73 ggtcaagcag aggggaagtgt ccaagtacca ggtatatcta tgatgatcct tcatcaagag 2760
 74 gtaagccacg accacggtaa aaagtaatag aaaa 2794

76 <210> SEQ ID NO: 2

77 <211> LENGTH: 958

78 <212> TYPE: PRT

79 <213> ORGANISM: B. deramificans

81 <220> FEATURE:

82 <221> NAME/KEY: VARIANT

83 <222> LOCATION: (1)...(956)

84 <223> OTHER INFORMATION: Xaa = Any Amino Acid

86 <220> FEATURE:

87 <221> NAME/KEY: VARIANT

88 <222> LOCATION: (957)...(957)

89 <223> OTHER INFORMATION: Xaa = gap of indeterminate length

91 <400> SEQUENCE: 2

92 Met Ala Lys Lys Leu Ile Tyr Val Cys Leu Ser Val Cys Leu Val Leu
 93 1 5 10 15
 94 Thr Trp Ala Phe Asn Val Lys Gly Gln Ser Ala His Ala Asp Gly Asn
 95 20 25 30
 96 Thr Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln
 97 35 40 45
 98 Pro Trp Ser Leu Trp Met Trp Pro Lys Asp Gly Gly Ala Glu Tyr
 99 50 55 60
 100 Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val Ala Ser Ala Asp
 101 65 70 75 80
 102 Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp
 103 85 90 95
 104 Trp Thr Lys Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly
 105 100 105 110
 106 Asn Glu Val Trp Leu Val Glu Gly Asn Ser Gln Ile Phe Tyr Asn Glu
 107 115 120 125
 108 Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu
 109 130 135 140
 110 Asp Ala Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu
 111 145 150 155 160

*Xaa can only represent
a single amino acid.*

*Per 1.822(d)(5)(e) of
new Sequence Rules,*

*"A sequence with a
gap or gaps shall be
presented as a plurality
of separate sequences,
with separate sequence
identifiers, with the
number of separate
sequences being equal in
number to the number of
continuous strings of
sequence data."*

*Since only one amino
acid follows gap, and
at least four amino acids
are needed for a sequence,
eliminate last amino acid.*

2/5/01

RAW SEQUENCE LISTING

DATE: 02/05/2001

PATENT APPLICATION: US/09/262,126A

TIME: 14:10:04

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Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02022001\I262126A.raw

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112 Gly Glu Gly Xaa Ser Gly Phe Thr Val His Asp Asp Thr Ala Asn Lys
 113 165 170 175
 114 Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val
 115 180 185 190
 116 Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp
 117 195 200 205
 118 Trp Ala Pro Asp Asn His Ser Thr Leu Leu Lys Lys Val Thr Asn Asn
 119 210 215 220
 120 Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr Lys
 121 225 230 235 240
 122 Val Ala Leu Asn Asp Ser Trp Asn Asn Ser Tyr Pro Ser Asp Asn Ile
 123 245 250 255
 124 Asn Leu Thr Val Pro Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile
 125 260 265 270
 126 Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro Asn Ala Asp
 127 275 280 285
 128 Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu
 129 290 295 300
 130 Gly Glu Asp Pro Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly
 131 305 310 315 320
 132 Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val Leu Asn Ser Ser Gln
 133 325 330 335
 134 Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala
 135 340 345 350
 136 Thr Thr Phe Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu
 137 355 360 365
 138 Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr Lys Ile Val Pro Met Thr
 139 370 375 380
 140 Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu
 141 385 390 395 400
 142 Asn Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr
 143 405 410 415
 144 Ala Val Asp Pro Tyr Ala Thr Ala Ile Ala Pro Asn Gly Thr Arg Gly
 145 420 425 430
 146 Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly Trp Asn Ser Asp
 147 435 440 445
 148 Lys His Ile Thr Pro Lys Asn Ile Glu Asp Glu Val Ile Tyr Glu Met
 149 450 455 460
 150 Asp Val Arg Asp Phe Ser Ile Asp Pro Asn Ser Gly Met Lys Asn Lys
 151 465 470 475 480
 152 Gly Lys Tyr Leu Ala Leu Thr Glu Lys Gly Thr Lys Gly Pro Asp Asn
 153 485 490 495
 154 Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu Gly Ile Thr His Val
 155 500 505 510
 156 Gln Leu Met Pro Val Phe Ala Ser Asn Ser Val Asp Glu Thr Asp Pro
 157 515 520 525
 158 Thr Gln Asp Asn Trp Gly Tyr Asp Pro Arg Asn Tyr Asp Val Pro Glu
 159 530 535 540
 160 Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg Ile Lys Glu Phe

RAW SEQUENCE LISTING

DATE: 02/05/2001

PATENT APPLICATION: US/09/262,126A

TIME: 14:10:04

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02022001\I262126A.raw

161 545 550 555 560
 162 Lys Glu Met Val Leu Ser Leu His Arg Glu His Ile Gly Val Asn Met
 163 565 570 575
 164 Asp Val Val Tyr Asn His Thr Phe Ala Thr Gln Ile Ser Asp Phe Asp
 165 580 585 590
 166 Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile
 167 595 600 605
 168 Pro Thr Asp Gln Val Leu Glu Met Lys Leu Xaa Ala Glu Arg Pro Met
 169 610 615 620
 170 Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr Trp Val Asn Glu Tyr
 171 625 630 635 640
 172 His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp
 173 645 650 655
 174 Thr Met Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile
 175 660 665 670
 176 Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Ala Leu Pro Asp
 177 675 680 685
 178 Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val
 179 690 695 700
 180 Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser
 181 705 710 715 720
 182 Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu Thr Asp Ala Ile
 183 725 730 735
 184 Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro Gly
 185 740 745 750
 186 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp
 187 755 760 765
 188 Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala Asp Arg Ile Lys
 189 770 775 780
 190 Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly Val Pro
 191 785 790 795 800
 192 Phe Met Gln Gly Gly Glu Glu Met Leu Arg Xaa Lys Gly Gly Asn Asp
 193 805 810 815
 194 Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg
 195 820 825 830
 196 Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly Leu Ile His
 197 835 840 845
 198 Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile
 199 850 855 860
 200 Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr
 201 865 870 875 880
 202 Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly Asn Ile Ile Val
 203 885 890 895
 204 Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly
 205 900 905 910
 206 Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu
 207 915 920 925
 208 Gly Gln Ala Glu Gly Ser Val Gln Val Pro Gly Ile Ser Met Met Ile
 209 930 935 940

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/262,126A

DATE: 02/05/2001
TIME: 14:10:04

Input Set : A:\GC396-2 seq.txt
Output Set: N:\CRF3\02022001\I262126A.raw

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TECH CENTER 1600/2000

W--> 210 Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys Xaa Lys
211 945 950 955

213 <210> SEQ ID NO: 3
214 <211> LENGTH: 718
215 <212> TYPE: PRT
216 <213> ORGANISM: B. subtilis
218 <400> SEQUENCE: 3

219 Met Val Ser Ile Arg Arg Ser Phe Glu Ala Tyr Val Asp Asp Met Asn
220 1 5 10 15
221 Ile Ile Thr Val Leu Ile Pro Ala Glu Gln Lys Glu Ile Met Thr Pro
222 20 25 30
223 Pro Phe Arg Leu Glu Thr Glu Ile Thr Asp Phe Pro Leu Ala Val Arg
224 35 40 45
225 Glu Glu Tyr Ser Leu Glu Ala Lys Tyr Lys Tyr Val Cys Val Ser Asp
226 50 55 60
227 His Pro Val Thr Phe Gly Lys Ile His Cys Val Arg Ala Ser Ser Gly
228 65 70 75 80
229 His Lys Thr Asp Leu Gln Ile Gly Ala Val Ile Arg Thr Ala Ala Phe
230 85 90 95
231 Asp Asp Glu Phe Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Thr Ala
232 100 105 110
233 Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
234 115 120 125
235 Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
236 130 135 140
237 Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
238 145 150 155 160
239 Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
240 165 170 175
241 Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
242 180 185 190
243 Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
244 195 200 205
245 Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
246 210 215 220
247 Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
248 225 230 235 240
249 Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Ser Gly
250 245 250 255
251 Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
252 260 265 270
253 Val Asn Asp Phe Ala Gly Val Asp Glu Glu Lys Pro Leu Asp Ala Tyr
254 275 280 285
255 Asn Trp Gly Tyr Asn Pro Leu His Phe Phe Ala Pro Glu Gly Ser Tyr
256 290 295 300
257 Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
258 305 310 315 320
259 Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
260 325 330 335

VERIFICATION SUMMARY

DATE: 02/05/2001

PATENT APPLICATION: US/09/262,126A

TIME: 14:10:05

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02022001\I262126A.raw

L:34 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:34 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:67 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2